

[illegible]

Glu Trp Ile Gly Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro
 65 70 75 80
 tcc ctc aag agt cga gtc acc ata tca gta gac acg tcc aag aac cag 288
 Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln
 85 90 95
 ttc tcc ctg aag ctg agc tct gtg acc gcc gcg gac acg gct gtg tat 336
 Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr
 100 105 110
 tac tgt gcg aga gaa ata gca gct cgt cct cac cga tac ttt gac tac 384
 Tyr Cys Ala Arg Glu Ile Ala Ala Arg Pro His Arg Tyr Phe Asp Tyr
 115 120 125
 tgg ggc cag gga acc ctg gtc acc gtc tcc tca 417
 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 130 135
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 <211> 139
 <212> PRT
 <213> Homo sapiens
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 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
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 Val Leu Ser Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys
 20 25 30
 Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe
 35 40 45
 Ser Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu
 50 55 60
 Glu Trp Ile Gly Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro
 65 70 75 80
 Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln
 85 90 95
 Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr
 100 105 110
 Tyr Cys Ala Arg Glu Ile Ala Ala Arg Pro His Arg Tyr Phe Asp Tyr

115

120

125

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
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<210> 3

<211> 351

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(351)

<220>

<221> sig_peptide

<222> (1)..(24)

<400> 3

ctc tgg ctc cca gat acc act gga gaa ata gtg atg acg cag tct cca 48
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gcc acc ctg tct gtg tct cca ggg gaa aga gcc acc ctc tcc tgc agg 96
 Ala Thr Leu Ser Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
 20 25 30

gcc agt cag agt gtt agc agc aac tta gcc tgg tac cag cag aaa cct 144
 Ala Ser Gln Ser Val Ser Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro
 35 40 45

ggc cag gct ccc agg ctc ctc atc tat ggt gca tcc acc agg gcc act 192
 Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala Thr
 50 55 60

ggt atc cca gcc agg ttc agt ggc agt ggg tct ggg aca gag ttc act 240
 Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
 65 70 75 80

ctc acc atc agc agc ctg cag tct gaa gat ttt gca gtt tat tac tgt 288
 Leu Thr Ile Ser Ser Leu Gln Ser Glu Asp Phe Ala Val Tyr Tyr Cys
 85 90 95

cag cag tat aat aac tgg cct ccg tac act ttt ggc cag ggg acc aag 336
 Gln Gln Tyr Asn Asn Trp Pro Pro Tyr Thr Phe Gly Gln Gly Thr Lys
 100 105 110

ctg gag atc aaa cga
 Leu Glu Ile Lys Arg
 115

351

<210> 4
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 20 25 30
 Ala Ser Gln Ser Val Ser Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro
 35 40 45
 Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala Thr
 50 55 60
 Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
 65 70 75 80
 Leu Thr Ile Ser Ser Leu Gln Ser Glu Asp Phe Ala Val Tyr Tyr Cys
 85 90 95
 Gln Gln Tyr Asn Asn Trp Pro Pro Tyr Thr Phe Gly Gln Gly Thr Lys
 100 105 110
 Leu Glu Ile Lys Arg
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 <212> DNA
 <213> Homo sapiens

<220>
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<400> 5
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gtg gta ttc ggc gga ggg acc aag ctg acc gtc cta ggt cag ccc 333
 Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro
 100 105 110

<210> 8
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 8
 Ser Ser Glu Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln
 1 5 10 15

Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala
 20 25 30

Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
 35 40 45

Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
 50 55 60

Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
 65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn Pro
 85 90 95

Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro
 100 105 110

seq "052060"